

Attorney Docket No.: DEX-0312  
Inventors: Salceda et al.  
Serial No.: 10/078,090  
Filing Date: February 14, 2002  
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#### REMARKS

Claims 1-17 are pending in the instant application. Claims 6 and 10-17 have been withdrawn from consideration and subsequently canceled without prejudice by Applicants in this amendment. Claim 1-5 and 7-9 have been rejected. Claim 1 has been amended. New claims 18 through 21 have been added. Support for these amendments is provided in the specification at pages 13-15, page 20, lines 8-11, and page 32, lines 1-20. Thus, now new matter is added by these amendments. Reconsideration is respectfully requested in light of these amendments and the following remarks.

#### I. Finality of Restriction Requirement

The Examiner has made final the Restriction Requirement mailed January 28, 2004. Thus, in an earnest effort to advance the prosecution of this case, Applicants have canceled without prejudice nonelected claims 6 and 10-17. In light of the finality of this Restriction Requirement, Applicants reserve the right to file a divisional application to the canceled subject matter.

With respect to the Examiner's denial of Applicants' request to include SEQ ID NO:47 because no common core structure is disclosed for SEQ ID NO:47 and 48, Applicants are providing

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herewith a sequence alignment of SEQ ID NO:47 and 48 clearly demonstrating the core structure which these sequence share. Reconsideration of inclusion of SEQ ID NO:47 within the instant claims is therefore respectfully requested.

## II. Priority to Provisional Application

Applicants are providing herewith evidence, as requested by the Examiner, in the form of a sequence alignment demonstrating that SEQ ID NO:40 of U.S. Provisional Application Serial No. 60/268,999 is identical to SEQ ID NO:47 of the instant application. Further, evidence is provided herewith in the form of a sequence alignment demonstrating the core sequence shared by SEQ ID NO:47 and SEQ ID NO:48 of the instant invention. The provided evidence clearly demonstrates that the elected invention was disclosed in U.S. Provisional Application Serial No. 60/268,999 and that the priority claim is valid.

## III. Objection to Claims

Claims 1-5 and 7-9 are objected to because they do not reflect the elected subject matter, namely SEQ ID NO:48 encoding polypeptide SEQ ID NO: 151.

Accordingly, in an earnest effort to advance the prosecution of this case, Applicants have amended the claims to be drawn to the elected sequences.

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Withdrawal of this objection is therefore respectfully requested.

IV. Rejection of Claims 1-5 and 7-9 under 35 U.S.C. 101 and 112

Claims 1-5 and 7-9 have been rejected under 35 U.S.C. 101 and 112 as the Examiner suggests that the claimed invention lacks patentable utility.

Applicants respectfully traverse these rejections.

Data from bioassays demonstrating the utility of the claimed nucleic acid sequences is set forth in the specification at pages 111 through 118. As shown therein, using the Psmam001.dc bioassay, the claimed nucleic acid sequences were identified as differentially expressed in breast ductal cancer as compared to other normal tissues. Further, using the Psmam005.dc bioassay, the claimed nucleic acid sequences were identified as differentially expressed in breast ductal cancer as compared to other gynecological cancers.

The case law on utility is quite clear; mere identification of a pharmacological activity of a claimed compound that is relevant to an asserted pharmacological use provides an immediate benefit to the public and thus satisfies the utility requirement. *Nelson v. Bowler*, 626 F.2d 853, 206 USPQ 881, 883 (CCPA 1980). Clearly identification of SEQ ID NO:48 and 47 as being

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differentially expressed in breast cancer tissue as compared to normal tissue and other gynecological cancers constitutes a pharmacological activity relevant to the asserted use as a diagnostic for breast cancer, thus satisfying the utility requirement with respect to these nucleic acid molecules.

Withdrawal of these rejections under 35 U.S.C. § 101 and §112, first paragraph, is therefore respectfully requested.

**V. Rejection of Claims 1-5 and 7-9 under 35 U.S.C. § 112, first paragraph - Written Description**

Claims 1-5 and 7-9 have been rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. The Examiner suggests that the exact sequence of SEQ ID NO:48 meets the written description requirements. However, the Examiner suggests that the claims encompass gene sequences, encoding sequences and so forth which do not meet the written description provision of 35 U.S.C. § 112, first paragraph. Further, the Examiner suggests that there is insufficient description in the specification for nucleotides having more than 60% identity.

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Applicants respectfully traverse this rejection.

At the outset, it is respectfully pointed out that claim 1 has been amended and part (d) relating to nucleic acid molecules with at least 60% identity has been deleted, thus mooted this aspect of the rejection.

Further, in addition to the teachings of the specification acknowledged by the Examiner to meet the written description requirements for SEQ ID NO:48, Applicants respectfully direct the Examiner to page 111-118 wherein ATCC deposit information for clones containing this sequence are described. In accordance with MPEP § 2163, reference to a deposit may also satisfy the written description requirement with respect to a claimed material. Deposit of this clone clearly demonstrates Applicants' possession of other elements included in DNA and places the public in possession as well.

Thus, the instant specification and the claims as amended meet the "essential goal" of the written description requirements of 35 U.S.C. § 112, first paragraph as set forth in MPEP § 2163.

Withdrawal of this rejection under 35 U.S.C. § 112, first paragraph, is therefore respectfully requested.

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**VI. Rejection of Claim 1-5 and 7-9 under 35 U.S.C. 112, first paragraph - Lack of Enablement**

Claims 1-5 and 7-9 have been rejected under 35 U.S.C. § 112, first paragraph, for lack of enablement. The Examiner has acknowledged the specification to be enabled for the nucleic acid sequence of SEQ ID NO:48 but does not provide enablement for polynucleotides having at least 60% identity to polynucleotides encoding SEQ ID NO:151.

Applicants respectfully traverse this rejection.

At the outset, Applicants respectfully disagree with the Examiner citation of Skolnick et al. as being relevant to the instant claimed invention. Teachings of Skolnick et al. relate to a protein, not nucleic acid molecules as set forth in the instant claims.

Further, as discussed in Section V, Applicants have deleted part (d) of claim 1 relating to nucleic acid molecules with at least 60% identity, thus mooted this rejection.

Withdrawal of this rejection is therefore respectfully requested.

**VII. Rejection of Claims 1-5 under 35 U.S.C. 102(a)**

Claims 1-5 have been rejected under 35 U.S.C. 102(a) as

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being anticipated by the sequence of Accession number BF953475 (01/2001) and the sequence of Accession number AL110228. The Examiner suggests that the referenced sequences show more than 95% similarity to regions of SEQ ID NO:48 of the instant invention. Thus, the Examiner suggests that these sequences would be expected to selectively hybridize to SEQ ID NO:48.

Further, claims 1-5 have been rejected under 35 U.S.C. 102(a) as being anticipated by the sequence of Accession number AB040959. The Examiner suggests that the referenced sequence has 96% identity to a polynucleotide encoding polypeptide SEQ ID NO:151.

Accordingly, in an earnest effort to advance the prosecution of this case, Applicants have amended part (c) of claim 1 in accordance with teachings at pages 13 through 15 of the specification to state that the nucleic acid molecule hybridizes under stringent conditions to a nucleic acid molecule of part (a) or part (b). Further, stringent hybridization conditions are defined specifically in the claim as conditions of 50% formamide/6X SSC at 42°C for at least 10 hours or 6X SSC at 68°C without formamide for at least 10 hours. Sequences of Accession number BF953475 (01/2001) and Accession number AL110228 would not hybridize under these stringent conditions and therefore do not

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meet the limitations of the claims as amended and thus cannot anticipate the claims as amended.

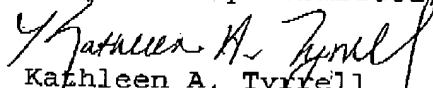
Further, Applicants have amended claim 1 to delete part (d) thus mooted the rejection over teachings of Accession number AB040959 with respect to percent identity.

Withdrawal of these rejections under 35 U.S.C. § 102(a) is therefore respectfully requested.

#### VIII. Conclusion

Applicants believe that the foregoing comprises a full and complete response to the Office Action of record. Accordingly, favorable reconsideration and subsequent allowance of the pending claims is earnestly solicited.

Respectfully submitted,

  
Kathleen A. Tyrrell  
Reg. No. 38,350

Date: August 19, 2004

LICATA & TYRRELL P.C.  
66 E. Main Street  
Marlton, New Jersey 08053  
(856) 810-1515



2. *Phylogenetic relationships*—The phylogenetic relationships among the 10 species were determined using the maximum parsimony method. The analysis was performed using the computer program PAUP 4.0 (Swofford, 1999). The heuristic search was performed with 1000 random starting trees, 1000 steps per tree, and 1000 iterations. The tree was collapsed using the parsimony criterion. The bootstrap values were calculated using 1000 replicates. The results were visualized using the computer program TreeView 1.6.6 (Rambaut, 1999).

Query: 1391 ctatcattacatagtagtataataataattattagagagatacacagaaaatatatagag 1450  
Sbjct: 381 ctatcattacatagtagtataataataattattagagagatacacagaaaatatatagag 440

Query: 1451 aagataacagtggttctctataaaaaaaaaaacagctgccctctctgcatagcttctaaca 1510  
Sbjct: 441 aagataacagtggttctctataaaaaaaaaaacagctgccctctctgcatagcttctaaca 500

Query: 1511 ctcagcaactctcgcagaaaagagcacaaaacgggagaaacaagaaacaaacgggagaca 1570  
Sbjct: 501 ctcagcaactctcgcagaaaagagcacaaaacgggagaaacaagaaacaaacgggagaca 560

Query: 1571 agactagagaaaacacaggacagcggacaaaaccacgtgagggagcaacaccagaggggc 1630  
Sbjct: 561 agactagagaaaacacaggacagcggacaaaaccacgtgagggagcaacaccagaggggc 620

Query: 1631 gaaccacattacccccacacacgtgaaaaagcgagaccaggggggaga 1677  
Sbjct: 621 gaaccacattacccccacacacgtgaaaaagcgagaccaggggggaga 667

Score = 41.1 bits (21), Expect = 0.67  
Identities = 40/47 (85%), Gaps = 1/47 (2%)  
Strand = Plus / Minus

Query: 1089 agagagagatgctttgggggtgtatttggcca-gaggccaccaggctg 1134  
Sbjct: 291 agacagacatgctctgcagtgatttggccagggtggccaccaggctg 245

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 44  
Number of Sequences: 0  
Number of extensions: 44  
Number of successful extensions: 44  
Number of sequences better than 10.0: 1  
length of query: 667  
length of database: 2,385,885,539  
effective HSP length: 24  
effective length of query: 643  
effective length of database: 2,385,885,515  
effective search space: 1534124386145  
effective search space used: 1534124386145  
T: 0  
A: 30  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)

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S2: 19 (37.2 bits)

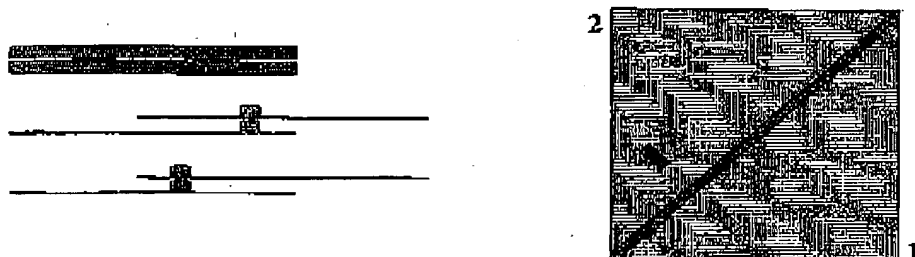
## BLAST 2 sequences

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☐

Sequence 1 lc|DEX0155\_40 Length 667 (1 .. 667)

Sequence 2 lc|DEX0312\_47 Length 667 (1 .. 667)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1283 bits (667), Expect = 0.0  
Identities = 667/667 (100%)  
Strand = Plus / Plus

Query: 1 gcgtggtcgcgggcccgaggtccataaacctgccctcatcccagatctgtgcagatgaaag 60  
Sbjct: 1 gcgtggtcgcgggcccgaggtccataaacctgccctcatcccagatctgtgcagatgaaag 60

Query: 61 agagggagggagaggggaaagagagagatgctttgggggtgtatttggccagaggccaccag 120  
Sbjct: 61 agagggagggagaggggaaagagagagatgctttgggggtgtatttggccagaggccaccag 120

Query: 121 gctggatcccatgaagaaatctgggtgagagggtcttaaagtcataaactgagatccagt 180  
Sbjct: 121 gctggatcccatgaagaaatctgggtgagagggtcttaaagtcataaactgagatccagt 180

Query: 181 tgccaggtggctgcatagttgccaacagtgtaatgtgtcaccttttgatcttcatcagaa 240  
Sbjct: 181 tgccaggtggctgcatagttgccaacagtgtaatgtgtcaccttttgatcttcatcagaa 240

Query: 241 atctcagcctggtggccacctggccaaatacactgcagagcatgtctgtctgtctgtctg 300  
Sbjct: 241 atctcagcctggtggccacctggccaaatacactgcagagcatgtctgtctgtctgtctg 300

Query: 301 tctgtgtctctctg 360  
Sbjct: 301 tctgtgtctctctg 360

Query: 361 tgtctcctcactcttttcctctatcattacatagtagtataataataaatattagagaga 420  
|||||  
Sbjct: 361 tgtctcctcactcttttcctctatcattacatagtagtataataataaatattagagaga 420

Query: 421 tacacagaaaatatatagagaagataaacagtgtttctctataaaaaaaaaaacagctgccct 480  
|||||  
Sbjct: 421 tacacagaaaatatatagagaagataaacagtgtttctctataaaaaaaaaaacagctgccct 480

Query: 481 ctctgcatagcttctaacaactcagcaactctcgagaaaagagcacaaaacgggagaaa 540  
|||||  
Sbjct: 481 ctctgcatagcttctaacaactcagcaactctcgagaaaagagcacaaaacgggagaaa 540

Query: 541 caagaaacaaacgggagacaagactagagaaaacacaggacagcggacaaaaccacgtga 600  
|||||  
Sbjct: 541 caagaaacaaacgggagacaagactagagaaaacacaggacagcggacaaaaccacgtga 600

Query: 601 gggagcaacaccagagggggcgaaccacattaccccacacacgtgaaaaagcgagaccagg 660  
|||||  
Sbjct: 601 gggagcaacaccagagggggcgaaccacattaccccacacacgtgaaaaagcgagaccagg 660

Query: 661 ggggaga 667  
|||||  
Sbjct: 661 ggggaga 667

Score = 41.1 bits (21), Expect = 0.67  
Identities = 40/47 (85%), Gaps = 1/47 (2%)  
Strand = Plus / Minus

Query: 245 cagcctgggtggccacctggccaaatacactgcagagcatgtctgtct 291  
|||||  
Sbjct: 124 cagcctgggtggcctc-tggccaaatacaccacaaagcatctctctct 79

Score = 41.1 bits (21), Expect = 0.67  
Identities = 40/47 (85%), Gaps = 1/47 (2%)  
Strand = Plus / Minus

Query: 79 agagagagatgctttgggggtgtatttggcca-gagggcaccaggctg 124  
||| ||| |||| || |||||  
Sbjct: 291 agacagacatgctctgcagtgatttggccaggtggccaccaggctg 245

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped  
Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 45

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Number of Sequences: 0  
Number of extensions: 45  
Number of successful extensions: 45  
Number of sequences better than 10.0: 1  
length of query: 667  
length of database: 2,385,885,539  
effective HSP length: 24  
effective length of query: 643  
effective length of database: 2,385,885,515  
effective search space: 1534124386145  
effective search space used: 1534124386145  
T: 0  
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S2: 19 (37.2 bits)